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PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/890,475

DATE: 01/22/2002

TIME: 16:34:40

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ENTERED

3 <110> APPLICANT: Johanson, Urban
 4 West, Joanne
 5 Dean, Caroline
 7 <120> TITLE OF INVENTION: Arabidopsis thaliana derived Frigida gene conferring late
 flowering
 9 <130> FILE REFERENCE: Mewburn
 11 <140> CURRENT APPLICATION NUMBER: US 09/890,475
 C--> 12 <141> CURRENT FILING DATE: 2001-11-13
 14 <150> PRIOR APPLICATION NUMBER: PCT/GB00/00197
 15 <151> PRIOR FILING DATE: 2000-01-25
 17 <150> PRIOR APPLICATION NUMBER: GB 9902660.1
 18 <151> PRIOR FILING DATE: 1999-02-05
 20 <160> NUMBER OF SEQ ID NOS: 58
 22 <170> SOFTWARE: PatentIn Ver. 2.1
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 25 <211> LENGTH: 609
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Artificial Sequence
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: Description of Artificial Sequence: FRI amino acid
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 35 1 5 10 15
 37 Asn Pro Leu Leu Gln Arg His Gln Ser Glu Gln Arg Arg Arg Glu Leu
 38 20 25 30
 40 Pro Lys Ile Val Glu Thr Glu Ser Thr Ser Met Asp Ile Thr Ile Gly
 41 35 40 45
 43 Gln Ser Lys Gln Pro Gln Phe Leu Lys Ser Ile Asp Glu Leu Ala Ala
 44 50 55 60
 46 Phe Ser Val Ala Val Glu Thr Phe Lys Arg Gln Phe Asp Asp Leu Gln
 47 65 70 75 80
 49 Lys His Ile Glu Ser Ile Glu Asn Ala Ile Asp Ser Lys Leu Glu Ser
 50 85 90 95
 52 Asn Gly Val Val Leu Ala Ala Arg Asn Asn Asn Phe His Gln Pro Met
 53 100 105 110
 55 Leu Ser Pro Pro Arg Asn Asn Val Ser Val Glu Thr Thr Val Thr Val
 56 115 120 125
 58 Ser Gln Pro Ser Gln Glu Ile Val Pro Glu Thr Ser Asn Lys Pro Glu
 59 130 135 140
 61 Gly Gly Arg Met Cys Glu Leu Met Cys Ser Lys Gly Leu Arg Lys Tyr
 62 145 150 155 160
 64 Ile Tyr Ala Asn Ile Ser Asp Gln Ala Lys Leu Met Glu Glu Ile Pro
 65 165 170 175

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67 Ser Ala Leu Lys Leu Ala Lys Glu Pro Ala Lys Phe Val Leu Asp Cys
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70 Ile Gly Lys Phe Tyr Leu Gln Gly Arg Arg Ala Phe Thr Lys Glu Ser
71      195      200      205
73 Pro Met Ser Ser Ala Arg Gln Val Ser Leu Leu Ile Leu Glu Ser Phe
74      210      215      220
76 Leu Leu Met Pro Asp Arg Gly Lys Gly Lys Val Lys Ile Glu Ser Trp
77 225      230      235      240
79 Ile Lys Asp Glu Ala Glu Thr Ala Ala Val Ala Trp Arg Lys Arg Leu
80      245      250      255
82 Met Thr Glu Gly Gly Leu Ala Ala Ala Glu Lys Met Asp Ala Arg Gly
83      260      265      270
85 Leu Leu Leu Leu Val Ala Cys Phe Gly Val Pro Ser Asn Phe Arg Ser
86      275      280      285
88 Thr Asp Leu Leu Asp Leu Ile Arg Met Ser Gly Ser Asn Glu Ile Ala
89      290      295      300
91 Gly Ala Leu Lys Arg Ser Gln Phe Leu Val Pro Met Val Ser Gly Ile
92 305      310      315      320
94 Val Glu Ser Ser Ile Lys Arg Gly Met His Ile Glu Ala Leu Glu Met
95      325      330      335
97 Val Tyr Thr Phe Gly Met Glu Asp Lys Phe Ser Ala Ala Leu Val Leu
98      340      345      350
100 Thr Ser Phe Leu Lys Met Ser Lys Glu Ser Phe Glu Arg Ala Lys Arg
101      355      360      365
103 Lys Ala Gln Ser Pro Leu Ala Phe Lys Glu Ala Ala Thr Lys Gln Leu
104      370      375      380
106 Ala Val Leu Ser Ser Val Met Gln Cys Met Glu Thr His Lys Leu Asp
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109 Pro Ala Lys Glu Leu Pro Gly Trp Gln Ile Lys Glu Gln Ile Val Ser
110      405      410      415
112 Leu Glu Lys Asp Thr Leu Gln Leu Asp Lys Glu Met Glu Glu Lys Ala
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115 Arg Ser Leu Ser Leu Met Glu Glu Ala Ala Leu Ala Lys Arg Met Tyr
116      435      440      445
118 Asn Gln Gln Ile Lys Arg Pro Arg Leu Ser Pro Met Glu Met Pro Pro
119      450      455      460
121 Val Thr Ser Ser Ser Tyr Ser Pro Ile Tyr Arg Asp Arg Ser Phe Pro
122 465      470      475      480
124 Ser Gln Arg Asp Asp Asp Gln Asp Glu Ile Ser Ala Leu Val Ser Ser
125      485      490      495
127 Tyr Leu Gly Pro Ser Thr Ser Phe Pro His Arg Ser Arg Arg Ser Pro
128      500      505      510
130 Glu Tyr Met Val Pro Leu Pro His Gly Gly Leu Gly Arg Ser Val Tyr
131      515      520      525
133 Ala Tyr Glu His Leu Ala Pro Asn Ser Tyr Ser Pro Gly His Gly His
134      530      535      540
136 Arg Leu His Arg Gln Tyr Ser Pro Ser Leu Val His Gly Gln Arg His
137 545      550      555      560
139 Pro Leu Gln Tyr Ser Pro Pro Ile His Gly Gln Gln Gln Leu Pro Tyr

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142 Gly Ile Gln Arg Val Tyr Arg His Ser Pro Ser Glu Glu Arg Tyr Leu
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146          595          600          605
148 Lys
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154 <211> LENGTH: 3761
155 <212> TYPE: DNA
156 <213> ORGANISM: Arabidopsis thaliana
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161 cttttgggtt catattaccg agcaagaacc gttatttgtg attagacatg ttataaacca 180
162 ctgctttagt gactatttaa aacaatatat tacatgtcgt aatcatgcaa cctaactatg 240
163 ttttcattaa tcaaatacaa agaataaaga gaaaagtgcg tagattcaat tatttggcat 300
164 agactcaaaa gagtgtatat atatctgact tttattaaat tattaaacac aaatacatat 360
165 tttcataagc aaaactataa aagccctaaa catataatga ttacctcaa ggaaaaagtc 420
166 gttttctcct acttaaaaga taggttactt cctaattaat atataattta tgtgaacttc 480
167 acaatataca gttcaataaa atttggtaat ttgaccgatt taaggagagt ggaaattagg 540
168 gcttctgcaa tcttttttct tcgccgcaat ctcatgtcca attatccacc gacgggtggc 600
169 gcgcaaccca caacgacggc gaatccactg ctgcagcgac atcaatctga acagcgacga 660
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171 tctaagcagc ctcaattttt gaaatccata gacgaattag ctgcgttttc agttgcagtg 780
172 gaaacattca aacgccattt cgatgatctt cagaagcaca tcgagtcaat cgaaaacgca 840
173 attgattcca aactcgagag taacggcggt gtctcgccg cgcggaacaa taatttccat 900
174 cagccgatgt tatcgctcc gcggaacaat gtatctgtag aaaccaccgt cactgtgagc 960
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184 tcacagtttc ttgtccctat ggtctcagg accatattct gttctcactc ggtgaatttc 1560
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195 ttgatataat tattttctca cagaagaag cggctacaaa gcagctagct gtgttatcat 2220
196 cagttatgca gtgtatggag actcacaagt tagatcctgc gaaagaacta ccaggatggc 2280

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199 accaacagat aaaacgtcca aggttgtcac ccattggaaat gccaccagta acttcttcat 2460
200 cgtattctcc tatctaccgt gatagaagct ttcttagtca aagagacgat gaccaagatg 2520
201 aaatatcagc tcttgtgagt agttacctcg gcccgtaaac atcttttcct catcgctcaa 2580
202 gaagatcccc ggaatatatg gttccacttc cacatggtgg gttaggaaga agtgtatatg 2640
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207 aataggagga atgtaaattt gtaacaaagc tttttgtttt tgcttaagtt agtcatttat 2940
208 ttaactccca acagtctcaa aatttaattt aatgtttggg gcttaagaat gcaaattttt 3000
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236 tattaattaa ttaaacacaa atacatattt tcataagcaa aactataaaa gccctaaaca 180
237 tataatgatt acctcaaagg aaaaagtcgt tttctcttac ttaaaagata ggttacttcc 240
238 taattaatat ataatttatg tgaacttcac aatatacagt tcaataaaat ttggtaattt 300
239 gaccgattta aggagagtgg aaattagggc ttctgcaatc ttttttcttc gccgcaatct 360
240 catgtccaat tatccaccga cgggtggcggc gcaaccacac acgacggcga atccactgct 420
241 gcagcgacat caatctgaac agcgacgaag agaattaccg aagattgtcg aaacagagtc 480
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248 catatacgcg aatatctctg atcaagctaa gttaatggaa gagattcctt cagctttgaa 900
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252 gattaaagat gaggcggaga cggctgctgt tgcttggagg aaaaggttga tgactgaagg 1140
253 aggattagct gcggctgaga aaatggatgc aagggggttg cttttactag ttgcttgttt 1200
254 tgggtgttct tcaaaacttta ggagtacaga tttgctggat ttgataagga tgagtggttc 1260
255 gaatgagatt gccggtgctt tgaagcggtc acagtttctt gtccctatgg tctcaggtat 1320
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257 tggcatggag gataagtttt cagctgctct agttctaact tcattcttaa agatgagcaa 1440
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259 tacaaagcag ctagctgtgt tatcatcagt tatgcagtgt atggagactc acaagttaga 1560
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280 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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VERIFICATION SUMMARY

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